

Roark

#2

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/726,899

DATE: 01/27/2001
TIME: 00:25:33

INPUT SET: S36328.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Bandman, Olga
6 Goli, Surya K.
7 Hillman, Jennifer L.
8
9 (ii) TITLE OF THE INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
10
11 (iii) NUMBER OF SEQUENCES: 12
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94304
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 09/726,899
29 (B) FILING DATE:
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/785,065
34 (B) FILING DATE:
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Billings, Lucy J.
38 (B) REGISTRATION NUMBER: 36,749
39 (C) REFERENCE/DOCKET NUMBER: PF-0187 US
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 415-855-0555
43 (B) TELEFAX: 415-845-4166
44 (C) TELEX:
45
46

RAW SEQUENCE LISTING
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47 (2) INFORMATION FOR SEQ ID NO:1:
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 264 amino acids

51 (B) TYPE: amino acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear
54

55 (vii) IMMEDIATE SOURCE:

56 (A) LIBRARY: Consensus

57 (B) CLONE: Consensus
5859 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 61 | Met | Ala | Ala | Ala | Ala | Val | Ala | Arg | Leu | Trp | Trp | Arg | Gly | Ile | Leu | Gly |
| 62 | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| 63 | Ala | Ser | Ala | Leu | Thr | Arg | Gly | Thr | Gly | Arg | Pro | Ser | Val | Leu | Leu | Leu |
| 64 | | | | 20 | | | | | 25 | | | | | 30 | | |
| 65 | Pro | Val | Arg | Arg | Glu | Ser | Ala | Gly | Ala | Asp | Thr | Arg | Pro | Thr | Val | Arg |
| 66 | | | 35 | | | | | 40 | | | | | 45 | | | |
| 67 | Pro | Arg | Asn | Asp | Val | Ala | His | Lys | Gln | Leu | Ser | Ala | Phe | Gly | Glu | Tyr |
| 68 | | 50 | | | | | 55 | | | | | 60 | | | | |
| 69 | Val | Ala | Glu | Ile | Leu | Pro | Lys | Tyr | Val | Gln | Gln | Val | Gln | Val | Ser | Cys |
| 70 | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| 71 | Phe | Asn | Glu | Leu | Glu | Val | Cys | Ile | His | Pro | Asp | Gly | Val | Ile | Pro | Val |
| 72 | | | | 85 | | | | | 90 | | | | | 95 | | |
| 73 | Leu | Thr | Phe | Leu | Arg | Asp | His | Thr | Asn | Ala | Gln | Phe | Lys | Ser | Leu | Val |
| 74 | | | | 100 | | | | | 105 | | | | | 110 | | |
| 75 | Asp | Leu | Thr | Ala | Val | Asp | Val | Pro | Thr | Arg | Gln | Asn | Arg | Phe | Glu | Ile |
| 76 | | | 115 | | | | | 120 | | | | | 125 | | | |
| 77 | Val | Tyr | Asn | Leu | Leu | Ser | Leu | Arg | Phe | Asn | Ser | Arg | Ile | Arg | Val | Lys |
| 78 | | 130 | | | | | 135 | | | | | 140 | | | | |
| 79 | Thr | Tyr | Thr | Asp | Glu | Leu | Thr | Pro | Ile | Glu | Ser | Ala | Val | Ser | Val | Phe |
| 80 | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| 81 | Lys | Ala | Ala | Asn | Trp | Tyr | Glu | Arg | Glu | Ile | Trp | Asp | Met | Phe | Gly | Val |
| 82 | | | | 165 | | | | | 170 | | | | | 175 | | |
| 83 | Phe | Phe | Ala | Asn | His | Pro | Asp | Leu | Arg | Arg | Ile | Leu | Thr | Asp | Tyr | Gly |
| 84 | | | | 180 | | | | | 185 | | | | | 190 | | |
| 85 | Phe | Glu | Gly | His | Pro | Phe | Arg | Lys | Asp | Phe | Pro | Leu | Ser | Gly | Tyr | Val |
| 86 | | | 195 | | | | | 200 | | | | | 205 | | | |
| 87 | Glu | Leu | Arg | Tyr | Asp | Asp | Glu | Val | Lys | Arg | Val | Val | Ala | Glu | Pro | Val |
| 88 | | 210 | | | | | 215 | | | | | 220 | | | | |
| 89 | Glu | Leu | Ala | Gln | Glu | Phe | Arg | Lys | Phe | Asp | Leu | Asn | Ser | Pro | Trp | Glu |
| 90 | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| 91 | Ala | Phe | Pro | Val | Tyr | Arg | Gln | Pro | Pro | Glu | Ser | Leu | Lys | Leu | Glu | Ala |
| 92 | | | | 245 | | | | | | 250 | | | | | 255 | |
| 93 | Gly | Asp | Lys | Lys | Pro | Asp | Ala | Lys | | | | | | | | |
| 94 | | | | 260 | | | | | | | | | | | | |

95
96 (2) INFORMATION FOR SEQ ID NO:2:
97

98 (i) SEQUENCE CHARACTERISTICS:

99 (A) LENGTH: 1023 base pairs

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100 (B) TYPE: nucleic acid
101 (C) STRANDEDNESS: single
102 (D) TOPOLOGY: linear

103
104 (vii) IMMEDIATE SOURCE:
105 (A) LIBRARY: Consensus
106 (B) CLONE: Consensus
107

108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
109

| | | | | | | | | |
|-----|-------|-----------|------------|------------|-------------|------------|------------|------|
| 110 | GA | AACTCTAAT | ACGAGCACTA | TAGGGAAAGC | TGGTAGCCTG | CAGGTACCGG | TCCGGAATTC | 60 |
| 111 | CC | GGGTCGAC | CCACGCGTCC | GCCGTGCCCT | TGGGGCTCCG | TGTCCTGCTG | TCTTTCCGTC | 120 |
| 112 | CG | CTGCCTAG | TCTGCATCTG | AGTAACATGG | CGGCGGCGGC | GGTAGCCAGG | CTGTGGTGGC | 180 |
| 113 | GCG | GATCTT | GGGGGCTCG | GCGCTGACCA | GGGGGACTGG | GCGACCCCTC | GTTCTGTTGC | 240 |
| 114 | TGCC | GGTGAG | GCGGGAGAGC | GCCGGGGCCG | ACACGCGCCC | CACTGTCAGA | CCACGGAATG | 300 |
| 115 | ATGT | GGCCCA | CAAGCAGCTC | TCAGCTTTTG | GAGAGTATGT | GGCTGAAATC | TTGCCCAAGT | 360 |
| 116 | ATGT | CCAACA | AGTTCAGGTG | TCCTGCTTCA | ATGAGTTAGA | GGTCTGTATC | CATCCTGATG | 420 |
| 117 | GCGT | CATCCC | AGTGCTGACT | TTCTCTCAGG | ATCACACCAA | TGCACAGTTC | AAATCTCTGG | 480 |
| 118 | TTGA | CTTGAC | AGCAGTGGAC | GTCCCAACTC | GGCAAACCCG | TTTTGAGATT | GTCTACAACC | 540 |
| 119 | TGTT | TGCTCT | GCGCTTCAAC | TCACGGATCC | GTGTGAAGAC | CTACACAGAT | GAGCTGACGC | 600 |
| 120 | CCATT | GAGTC | TGCTGTCTCT | GTGTTCAAGG | CAGCCAACTG | GTATGAAAGG | GAGATCTGGG | 660 |
| 121 | ACAT | GTTTGG | AGTCTTCTTT | GCTAACCACC | CTGATCTAAG | AAGGATCCTG | ACAGATTATG | 720 |
| 122 | GCTT | CGAGGG | ACATCCTTTC | CGGAAAGACT | TTCTCTATATC | TGGCTATGTT | GAGTTACGTT | 780 |
| 123 | ATGA | TGATGA | AGTGAAGCGT | GTGGTGGCAG | AGCCGGTGGA | GTTGGCCCAA | GAGTTCCGCA | 840 |
| 124 | AATTT | GACCT | GAACAGCCCC | TGGGAGGCTT | TCCCAGTCTA | TCGCCAACCC | CCGGAGAGTC | 900 |
| 125 | TCAAG | CTTGA | AGCCGGAGAC | AAGAAGCCTG | ATGCCAAGTA | GCTCCAGGGA | ACGCATGTGG | 960 |
| 126 | ATCCT | AGACA | GCGCCTTATC | TATGATTGAG | TGTCCGTGTA | AATAAATTCC | TACTTAGACT | 1020 |
| 127 | TAC | | | | | | | 1023 |

128
129 (2) INFORMATION FOR SEQ ID NO:3:
130

131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 129 amino acids
133 (B) TYPE: amino acid
134 (C) STRANDEDNESS: single
135 (D) TOPOLOGY: linear
136

137 (vii) IMMEDIATE SOURCE:
138 (A) LIBRARY: Consensus
139 (B) CLONE: Consensus
140

141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
142

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 143 | Met | Ser | Phe | Pro | Lys | Tyr | Lys | Pro | Ser | Ser | Leu | Arg | Thr | Leu | Pro | Glu |
| 144 | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| 145 | Thr | Leu | Asp | Pro | Ala | Glu | Tyr | Asn | Ile | Ser | Pro | Glu | Thr | Arg | Arg | Ala |
| 146 | | | | 20 | | | | | 25 | | | | | 30 | | |
| 147 | Gln | Ala | Glu | Arg | Leu | Ala | Ile | Arg | Ala | Gln | Leu | Lys | Arg | Glu | Tyr | Leu |
| 148 | | | 35 | | | | | 40 | | | | | 45 | | | |
| 149 | Leu | Gln | Tyr | Asn | Asp | Pro | Asn | Arg | Arg | Gly | Leu | Ile | Glu | Asn | Pro | Ala |
| 150 | | 50 | | | | | 55 | | | | | 60 | | | | |
| 151 | Leu | Leu | Arg | Trp | Ala | Tyr | Ala | Arg | Thr | Ile | Asn | Val | Tyr | Pro | Asn | Phe |
| 152 | 65 | | | | | 70 | | | | 75 | | | | | 80 | |

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```

153 Arg Pro Thr Pro Lys Asn Ser Leu Met Gly Ala Leu Cys Gly Phe Gly
154                               85                               90                               95
155 Pro Leu Ile Phe Ile Tyr Tyr Ile Ile Lys Thr Glu Arg Asp Arg Lys
156                               100                               105                               110
157 Glu Lys Leu Ile Gln Glu Gly Lys Leu Asp Arg Thr Phe His Leu Ser
158                               115                               120                               125
159 Tyr
160
161

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

176 CCAAGATGTC GTTCCCAAAG TATAAGCCGT CGAGCCTGCG CACTCTGCCT GAGACCCTCG      60
177 ACCCAGCCGA ATACAACATA TCTCCGGAAA CCCGGCGGGC GCAAGCGGAG CGGTTGGCCA      120
178 TAAGAGCCCA GCTGAAACGA GAGTACCTGC TTCAGTACAA CGATCCCAAC CGCCGAGGGC      180
179 TCATCGAAAA TCCTGCCTTG CTTCGTTGGG CCTATGCAAG AACAATAAAT GTCTATCCTA      240
180 ATTTTCAGACC CACTCCTAAA AACTCACTCA TGGGAGCTCT GTGTGGATT TGGGCCCTCA      300
181 TCTTCATTTA TTATATTATC AAAACTGAGA GGGATAGGAA AGAAAACTT ATCCAGGAAG      360
182 GAAAATTGGA TCGAACATT CACCTCTCAT ATTAAGTCTG GCAATGATGA CTATATGTAT      420
183 TCCTGCCTAA ATAAATCATC TATTAATCAT T                                     451
184

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

199 Met Pro Phe Leu Asp Ile Gln Lys Arg Phe Gly Leu Asn Ile Asp Arg
200   1           5           10           15
201 Trp Leu Thr Ile Gln Ser Gly Glu Gln Pro Tyr Lys Met Ala Gly Arg
202           20           25           30
203 Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly Ile Gly
204           35           40           45
205 Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp Phe Val

```

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```

206          50          55          60
207  Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr Ile Arg
208  65          70          75          80
209  Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro Pro Pro
210          85          90          95
211  His His Ile Gly Lys Gly Glu Pro Arg Pro
212          100          105
213

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

228  AGCTAGTCGT TCTGAAGCGG CGGCCAGAGA AGAGTCAAGG GCACGAGCAT CGGCCATGCC      60
229  TTTCTTGGAC ATCCAGAAAA GGTTCCGCCCT TAACATAGAT CGATGGTTGA CAATCCAGAG      120
230  TGGTGAACAG CCCTACAAGA TGGCTGGTTCG ATGCCATGCT TTTGAAAAAG AATGGATAGA      180
231  ATGTGCACAT GGAATCGGTT ATACTCGGGC AGAGAAAGAG TGCAAGATAG AATATGATGA      240
232  TTTCTGTAGAG TGTTTGCTTC GGCAGAAAAC GATGAGACGT GCAGGTACCA TCAGGAAGCA      300
233  GCGGGATAAG CTGATAAAGG AAGGAAAGTA CACCCCTCCA CCTCACCACA TTGGCAAGGG      360
234  GGAGCCTCGG CCCTGAACAG AGCAGCTGCT GATGTCTGGA GGCTGATTTT CCTGTTCTCT      420
235  GTTCTCCACT GGAAAGGTTG TTTACGACAA ACCTCCTTGT CAAAGTGTGT      470
236

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

251  Met Ile Ala Arg Arg Asn Pro Glu Pro Leu Arg Phe Leu Pro Asp Glu
252  1          5          10          15
253  Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
254          20          25          30
255  Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
256          35          40          45
257  Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Xaa Xaa Tyr Ile
258  50          55          60

```

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/726,899

DATE: 01/27/2001
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| Line | Error | Original Text |
|------|-------|---------------|
|------|-------|---------------|

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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/726,899

DATE: 01/27/2001
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INPUT SET: S36328.raw

< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/726,899

DATE: 01/27/2001
TIME: 00:25:35

INPUT SET: S36328.raw

| Line | Original Text | Corrected Text |
|------|---|---|
| 3 | (1) General Information | (1) GENERAL INFORMATION: |
| 9 | (ii) TITLE OF THE INVENTION: NOVEL SUBUNITS O | (ii) TITLE OF INVENTION: NOVEL SUBUNITS OF NA |